

Fig. 1

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Gene	Primers and Probe			Amplicon bp
ZNF185	FP	TGG ATG AAA GGC AAG GTA AAG AG		84
	RP	TTC TAA AAC TCC CTT AAA GGC AGA CT		
	Probe	CCA AGA TAG GCT GGC TTC CCC CG		
PSP94	FP	AGT GAA TGG ATA ATC TAG TGT GCT TCT AGT		100
	RP	GCA TGG CTA CAC AAT CAT TGA CTA T		
	Probe	CCC AGG CCA GGC CTC ATT CTC CT		
BPAG1	FP	TCG CTG AAA GAG CAC GTC AT		94
	RP	AGC AAT CTA AAA CAC TGC AGC TTG		
	Probe	AAT CAA AGA GAA AGA TAT AAA TTC GTT CCC ACA GCC		
Erg-2	FP	TCC TGT CGG ACA GCT CCA AC		75
	RP	CGG GAT CCG TCA TCT TGA		
	Probe	TGC ATC ACC TGG GAA GGC ACC AAC		

Fig. 2a

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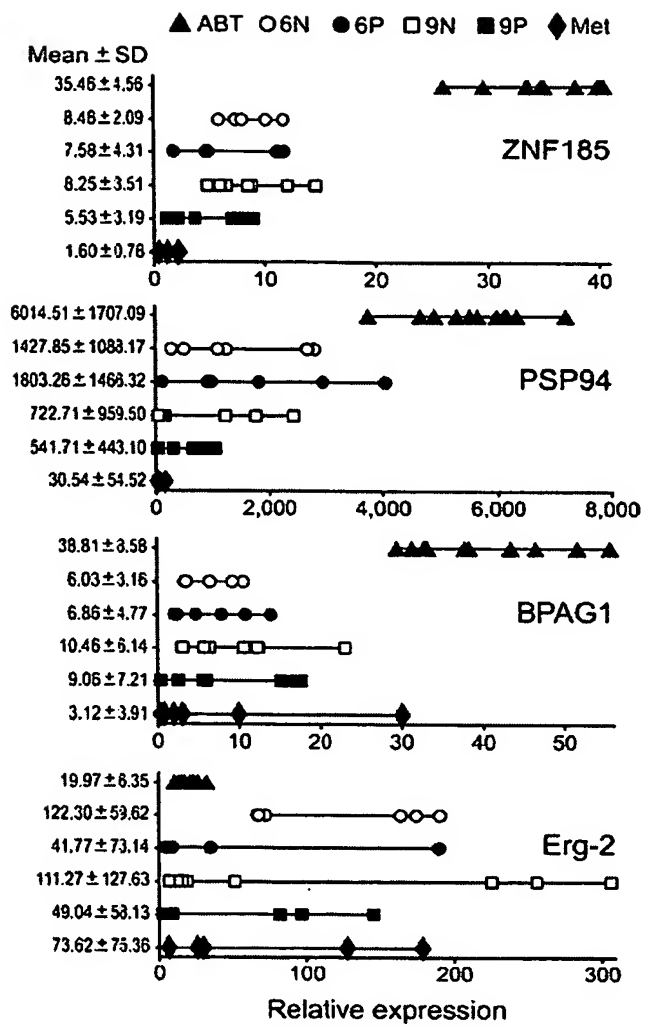


Fig. 2b

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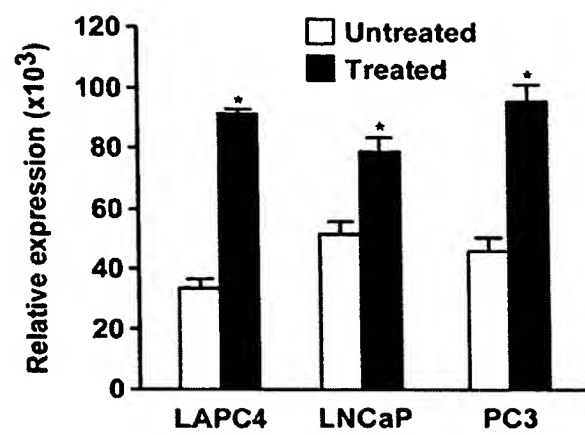


Fig. 3a

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Primer set			Size (bp)	Genomic position
1 W	FP	GCGCAGTTCGGGTGCTGTCTC	197	210
	RP	GCGGGGAGGACCAGCGTTAG		
1 M	FP	GCGTAGTTTCGGGTGTTTG	197	210
	RP	ACGAAAAAACAACCTTAACATA		
1 U	FP	GCTAGTTTGGGTGTTGTTAGG	198	210
	RP	CAAAAAACAACCTTAACATTCTC		
2 W	FP	CCTGGGACTCCGTCA GACTGG	148	335
	RP	GACAGACACCCGGAAC TGCG		
2 M	FP	TGGGATTTGTTAGATTGG	145	335
	RP	AACAACACCCGAAACTACG		
2 U	FP	TGGGATTTGTTAGATTGGAAAGG	146	333
	RP	CTAACAACACCCAAACTACACCA		

Fig. 3b

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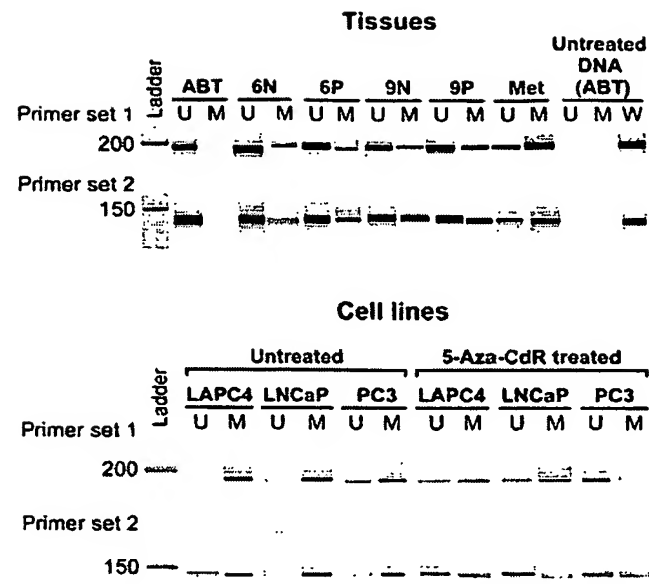


Fig. 3c

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Samples	Total	Methylated (%)
Benign prostatic tissues	12	0 (0)
Gleason Score 6 tumors	11	4 (36.3)
Gleason Score 9 tumors	14	7 (50)
Metastatic tissues	5	5 (100)

Fig. 3d

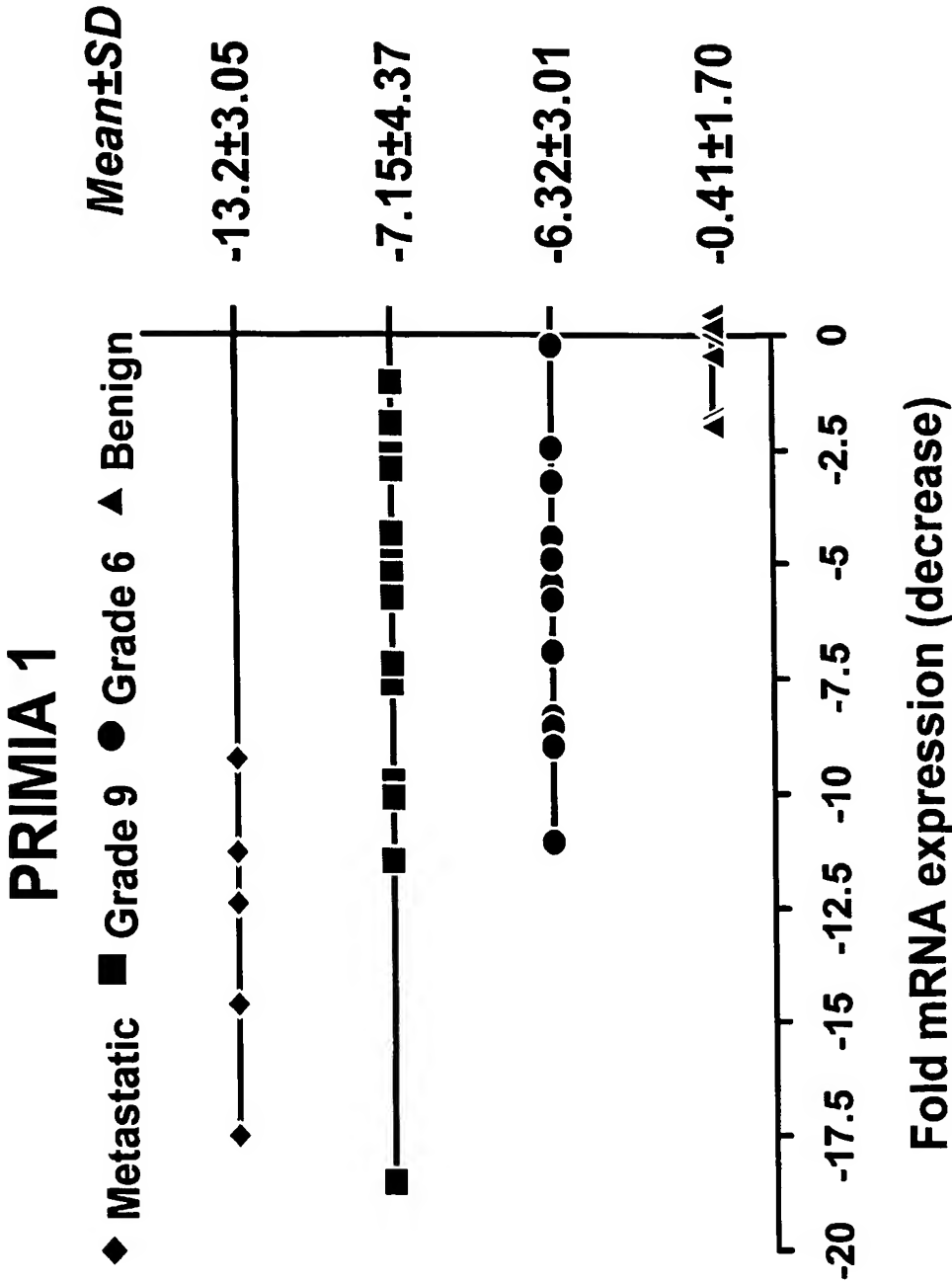
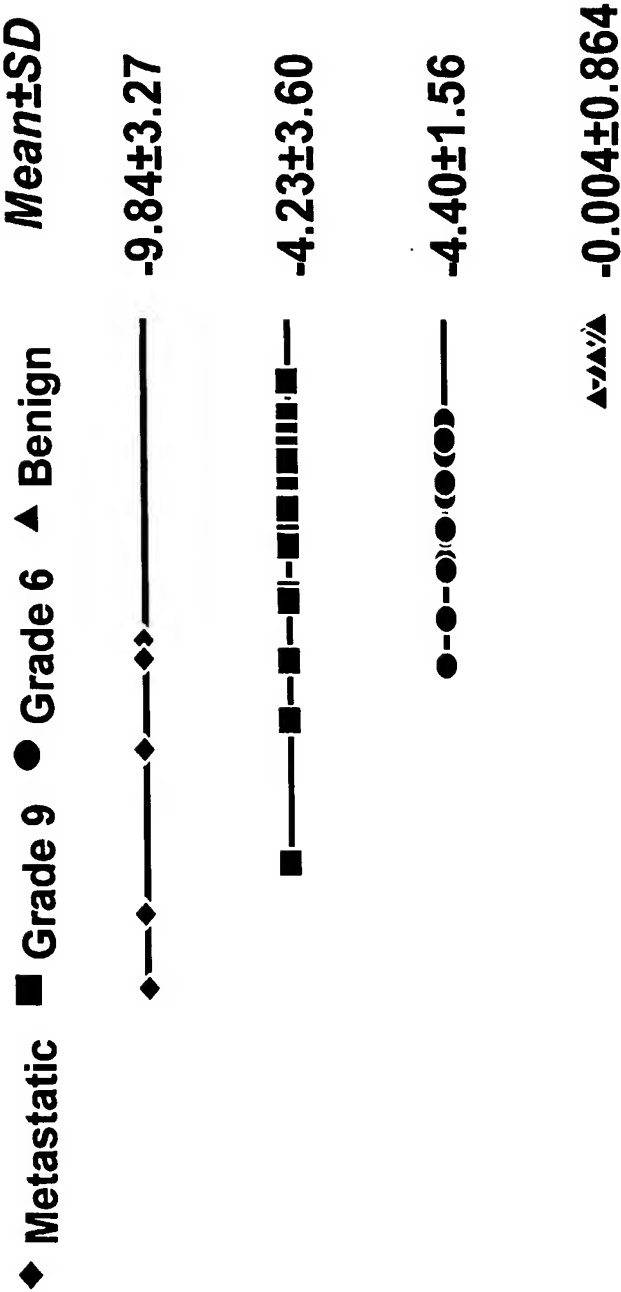


Fig. 4



Fold mRNA expression (decrease)

Fig. 5

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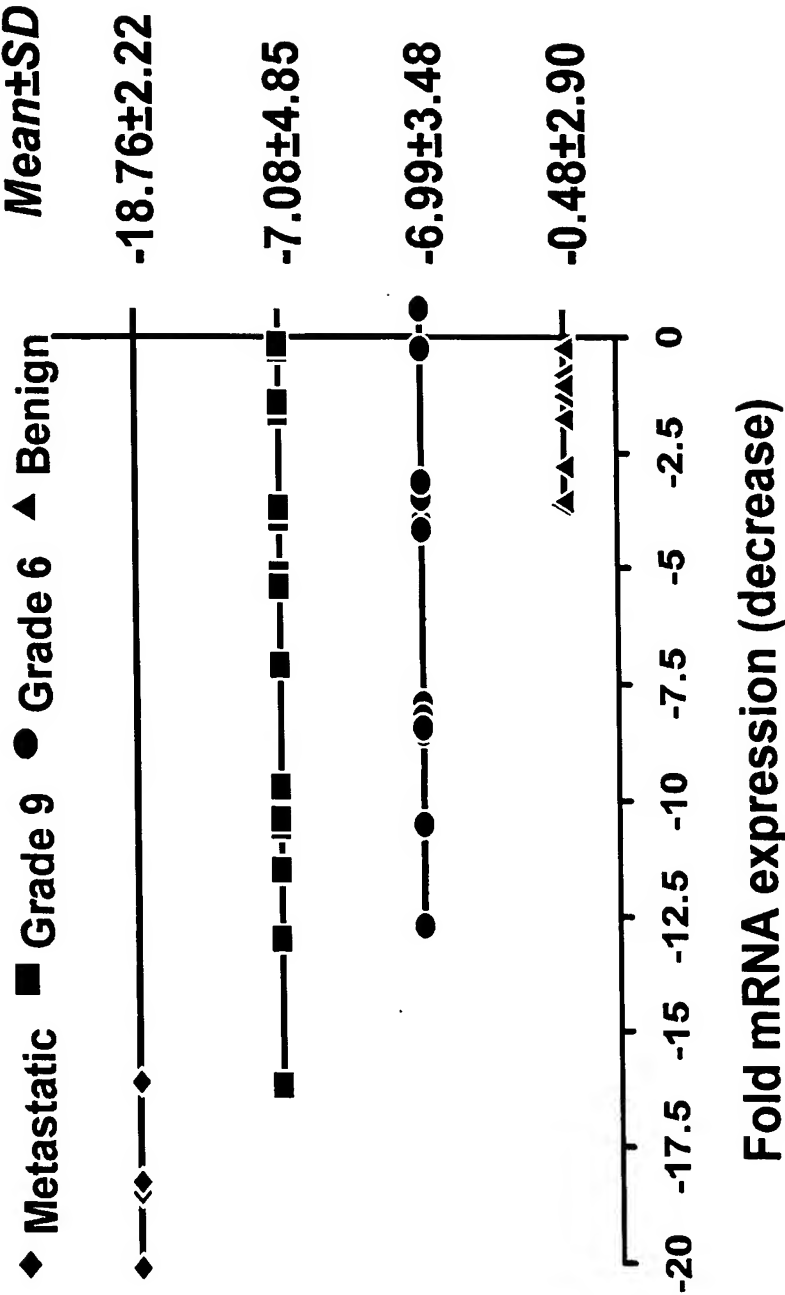


Fig. 6

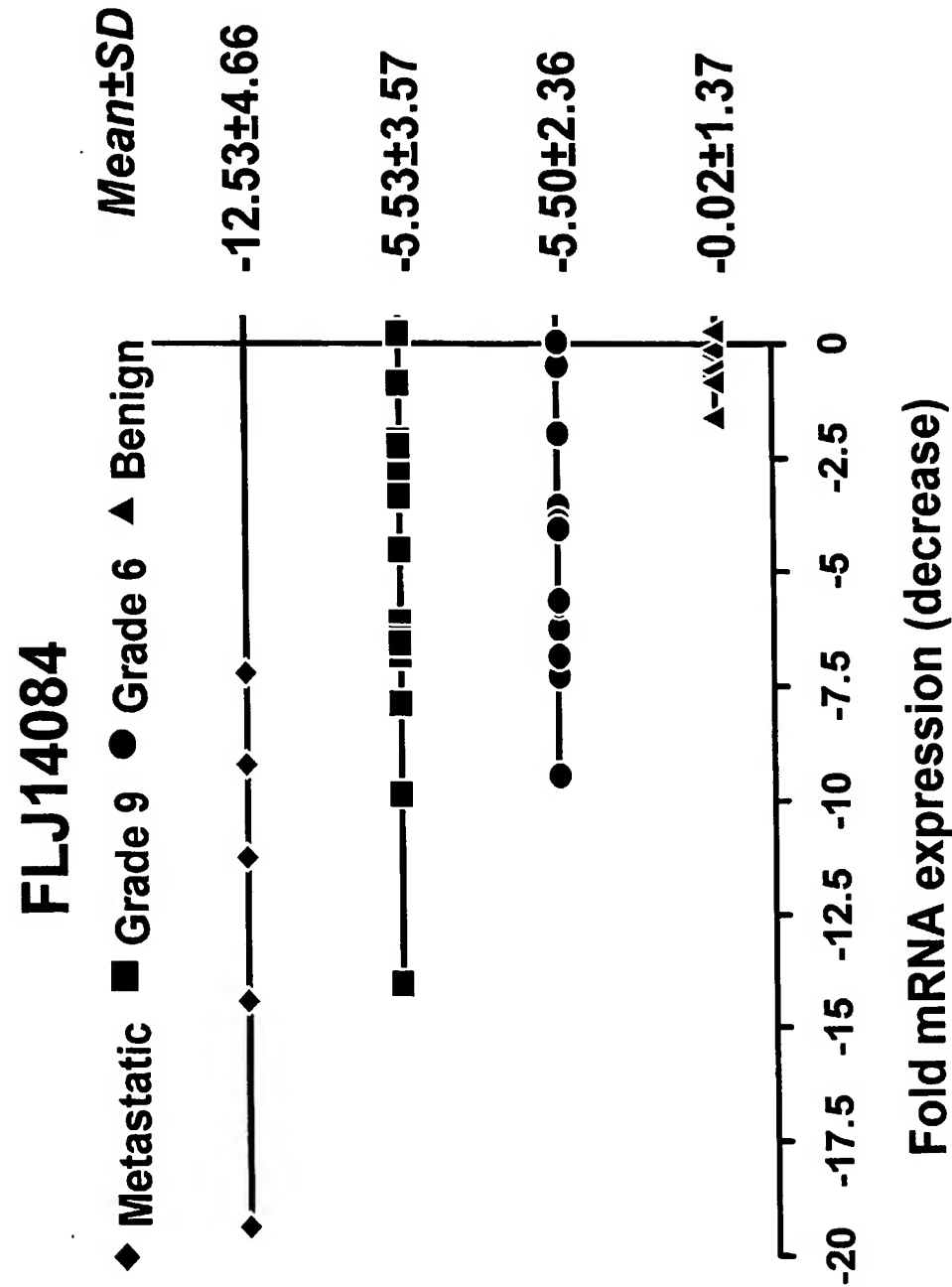
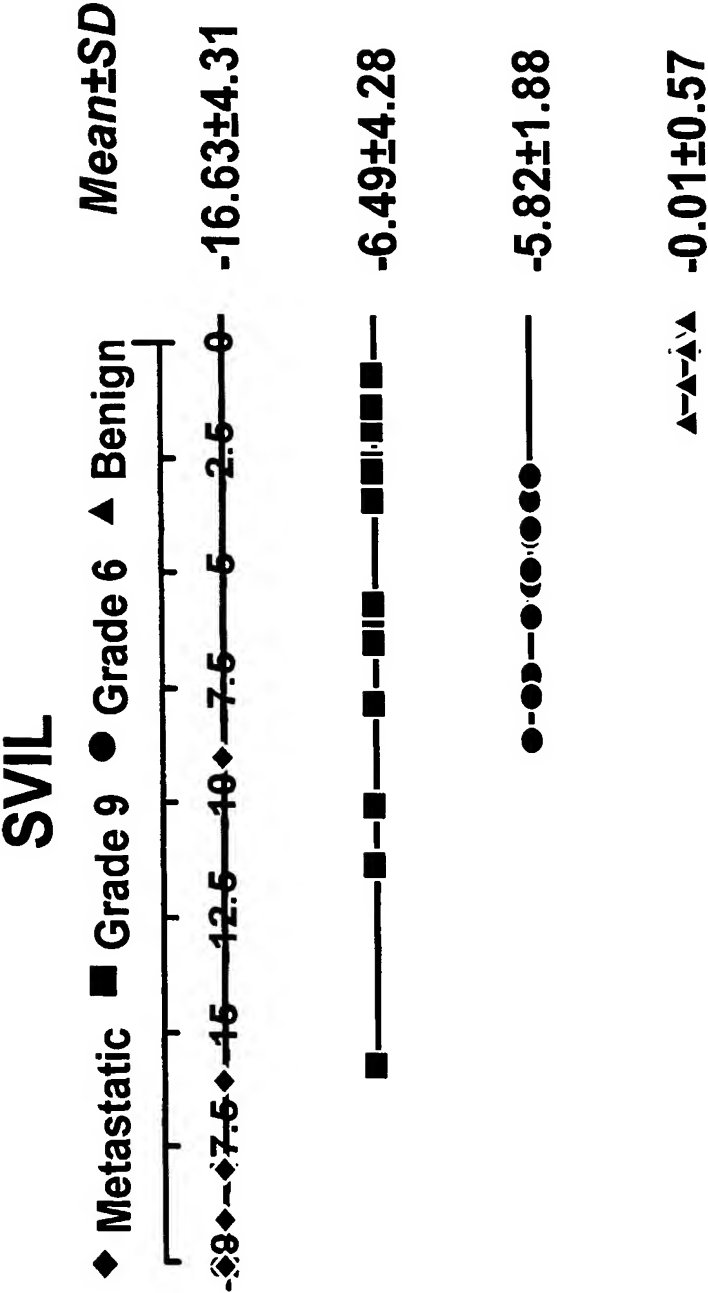


Fig. 7



Fold mRNA expression (decrease)

Fig. 8

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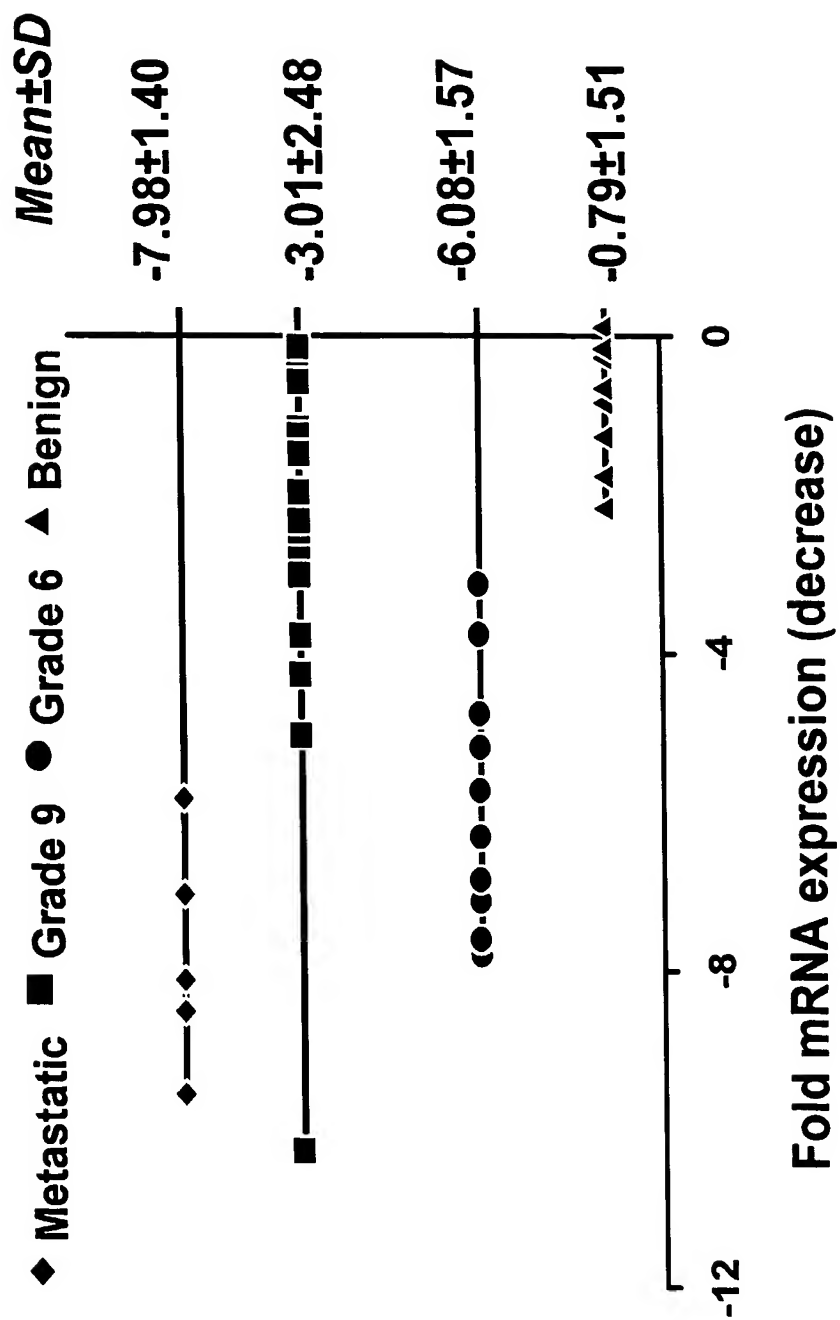


Fig. 9

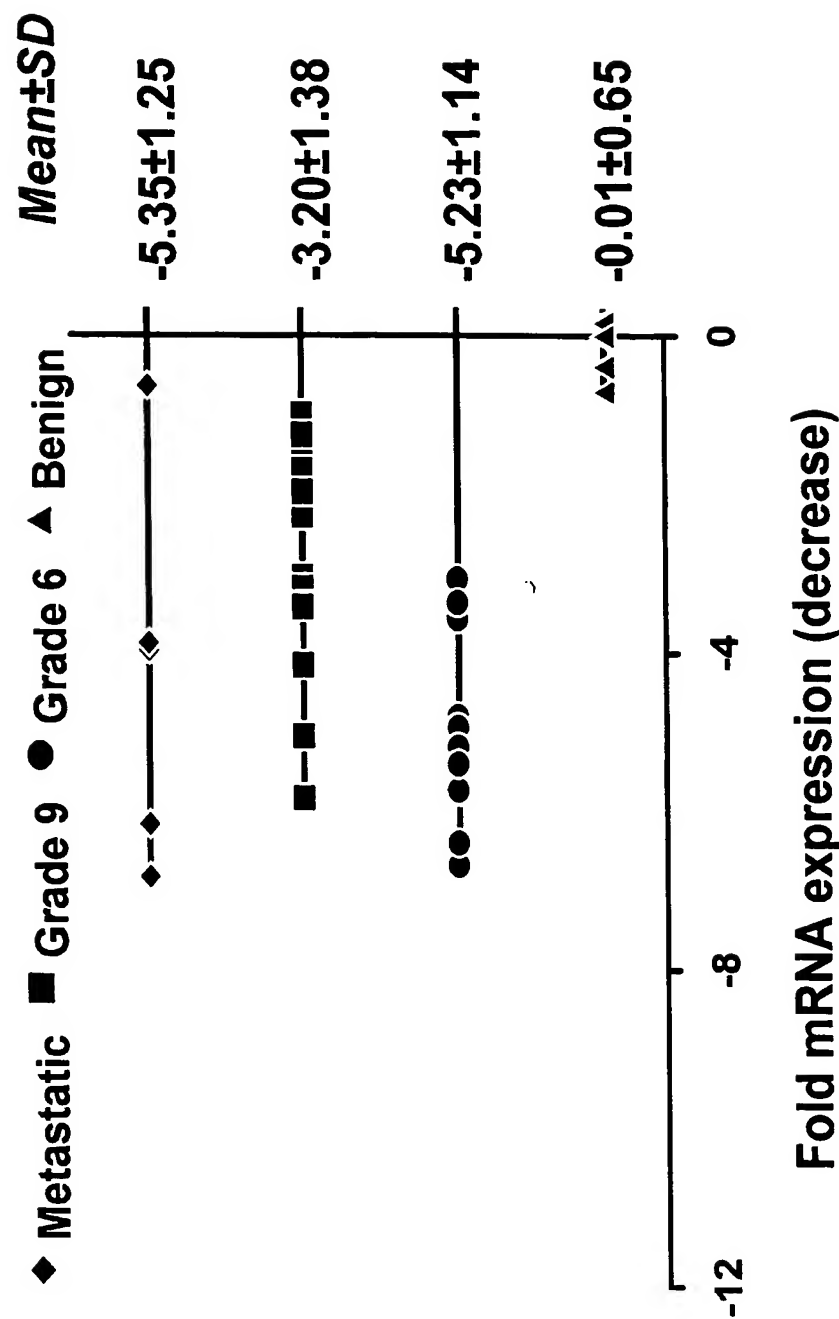


Fig. 10

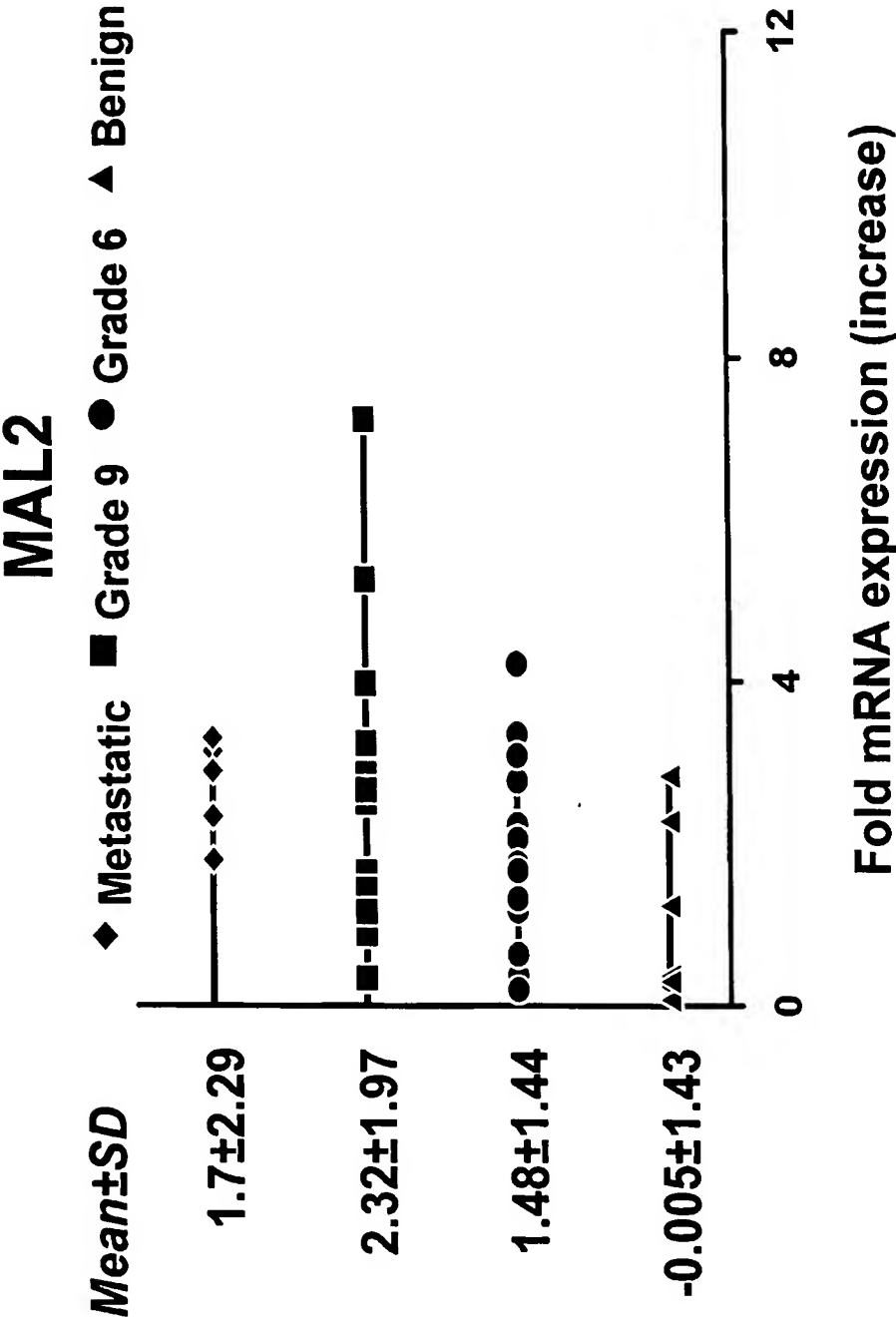


Fig. 11

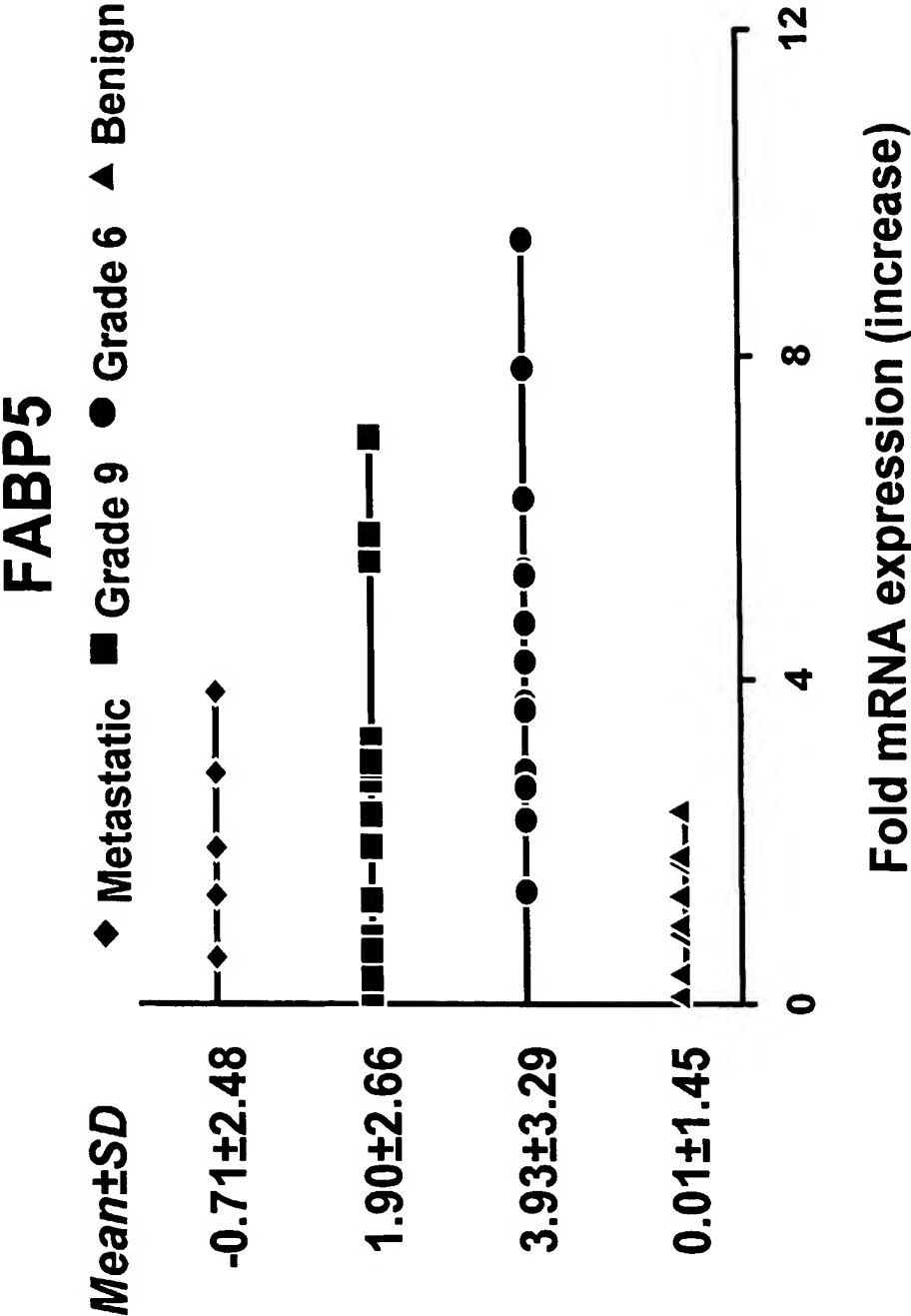


Fig. 12

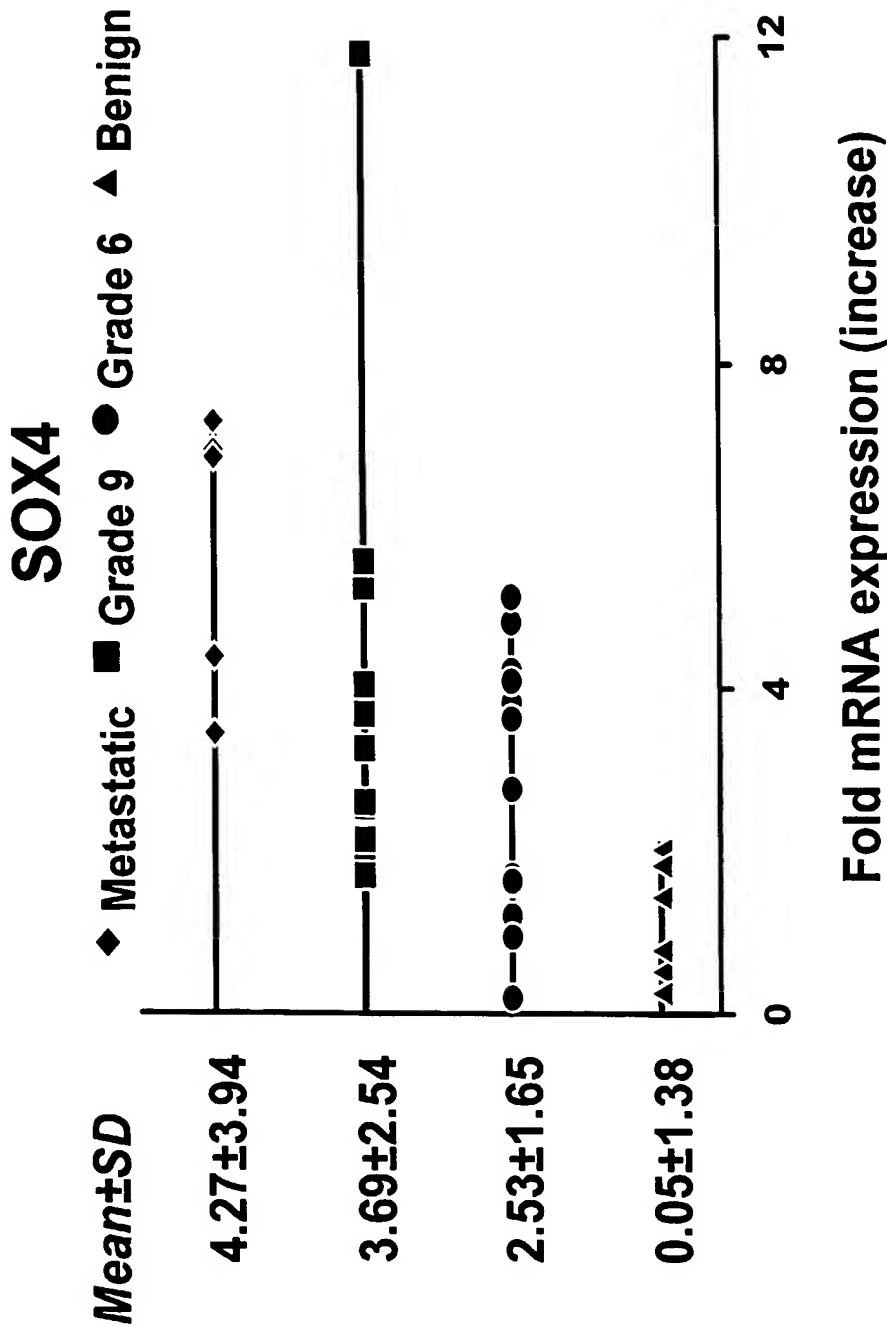


Fig. 13

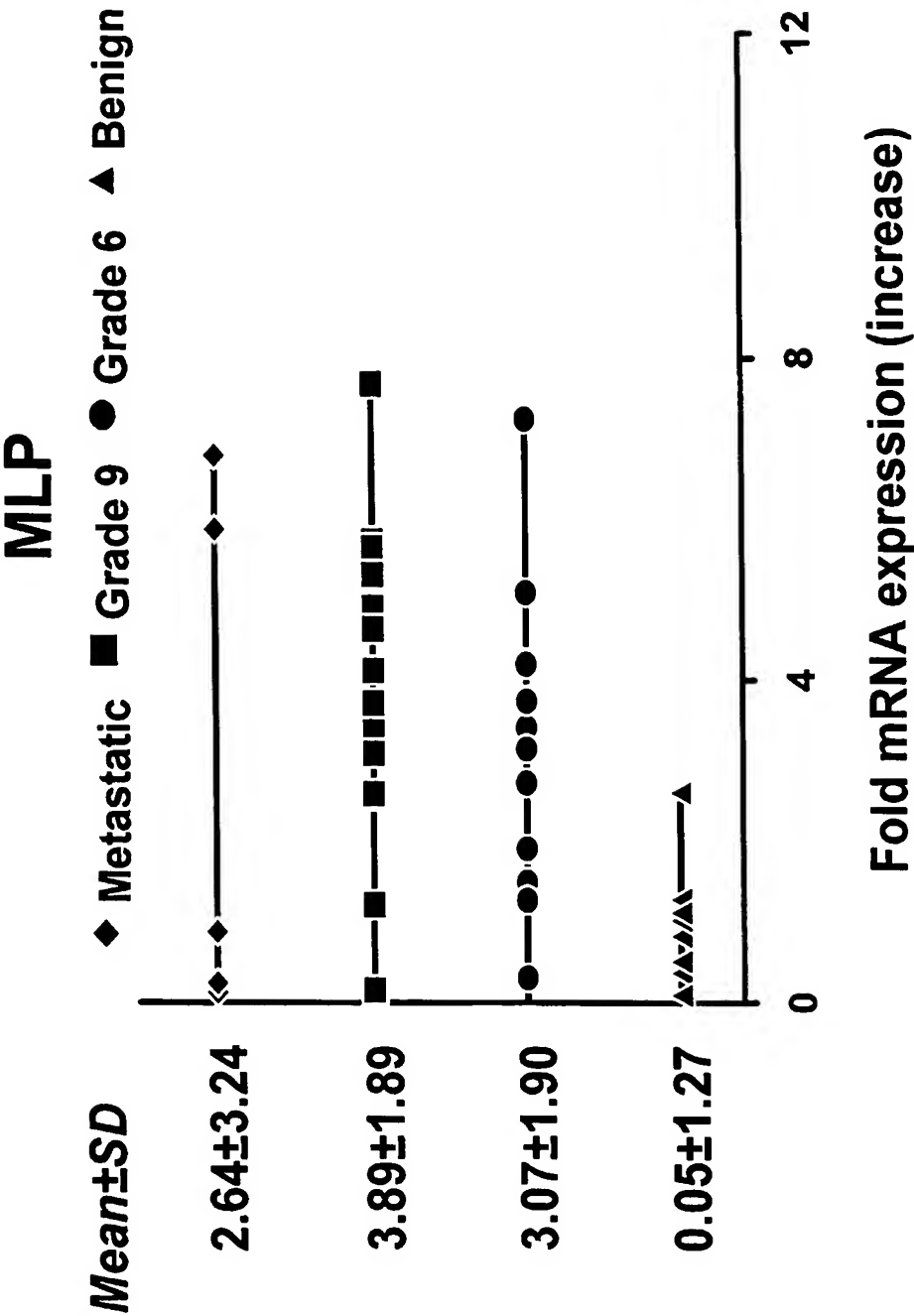


Fig. 14

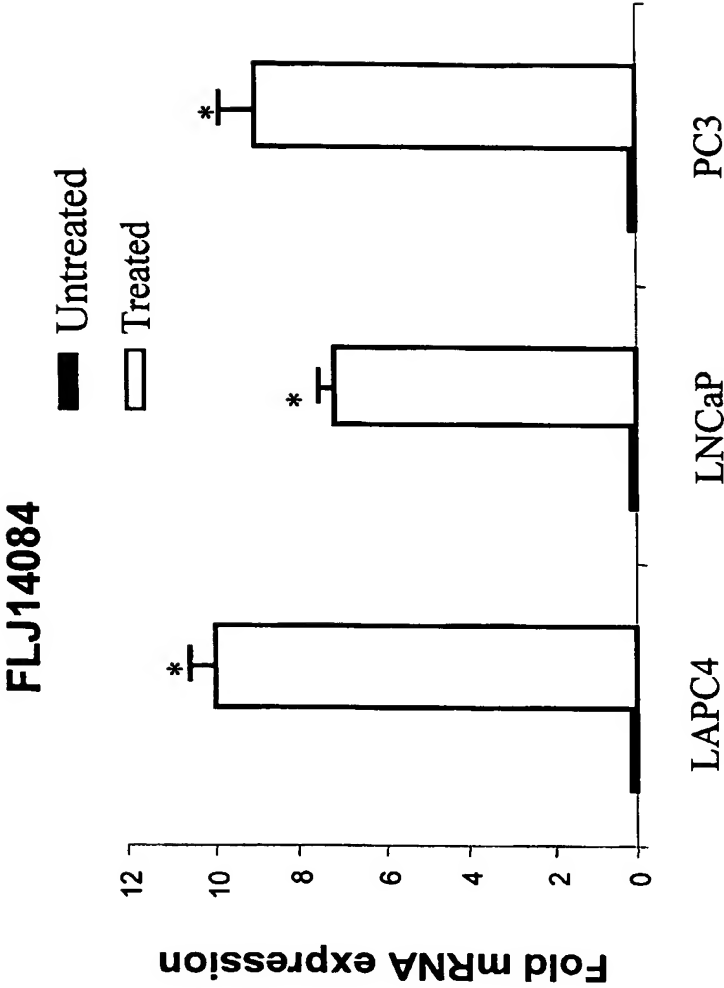


Fig. 15

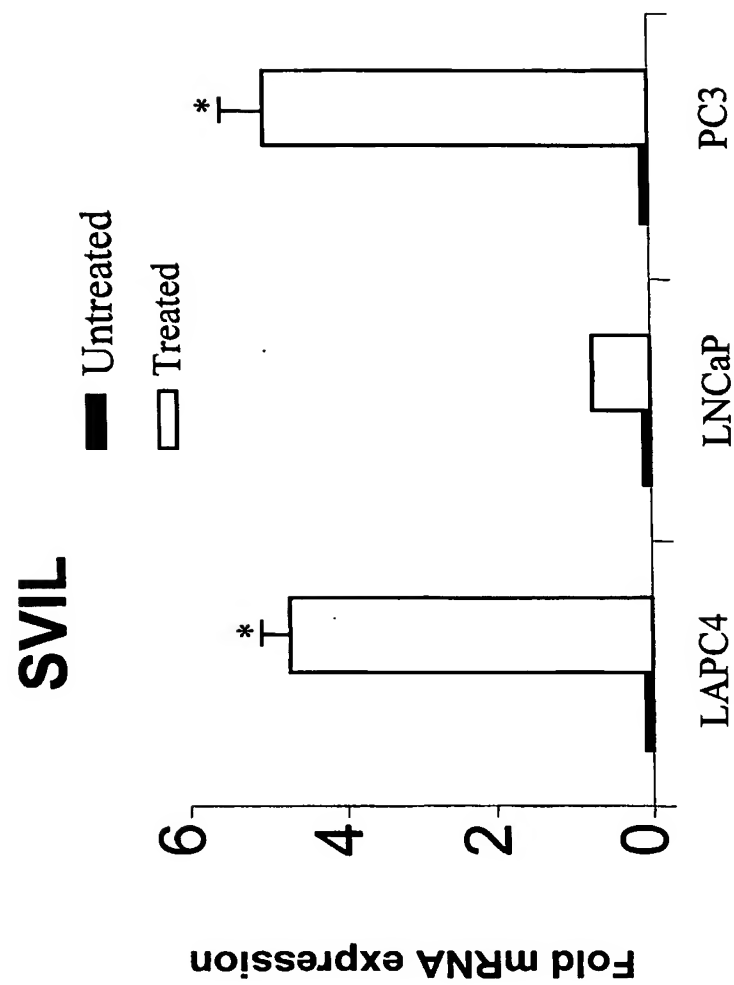


Fig. 16

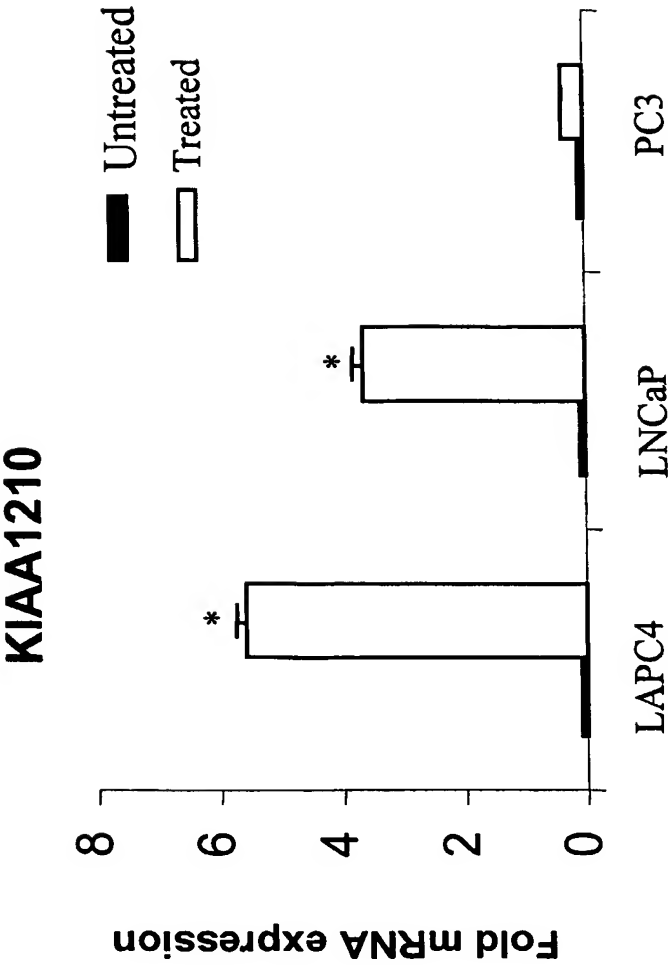


Fig. 17

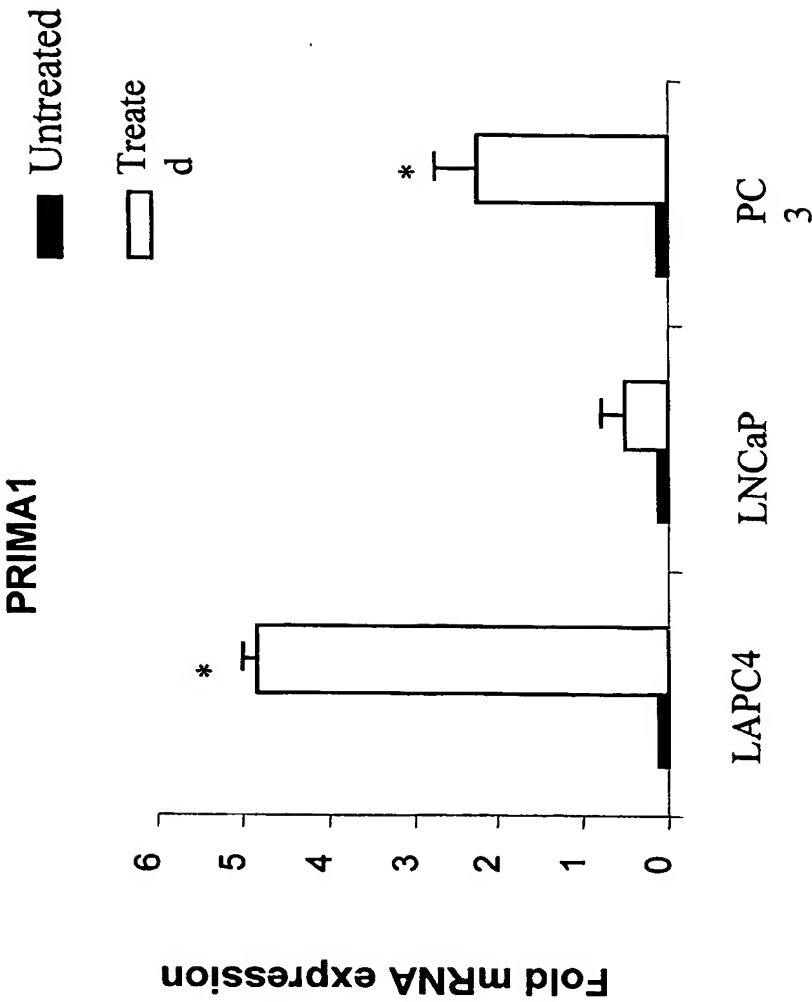


Fig. 18

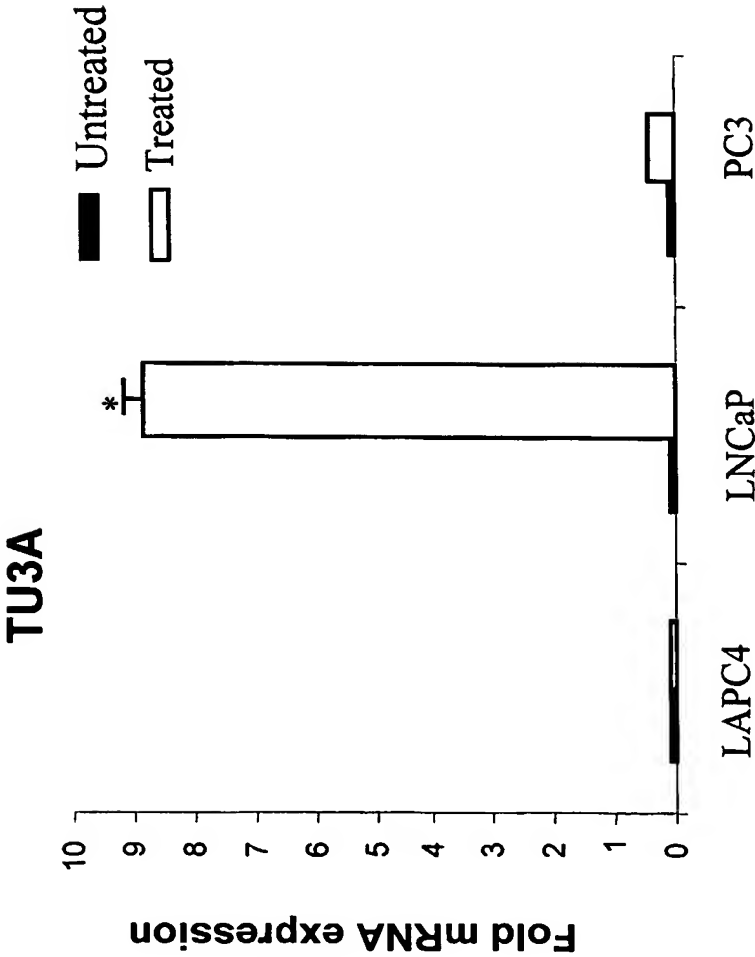


Fig. 19